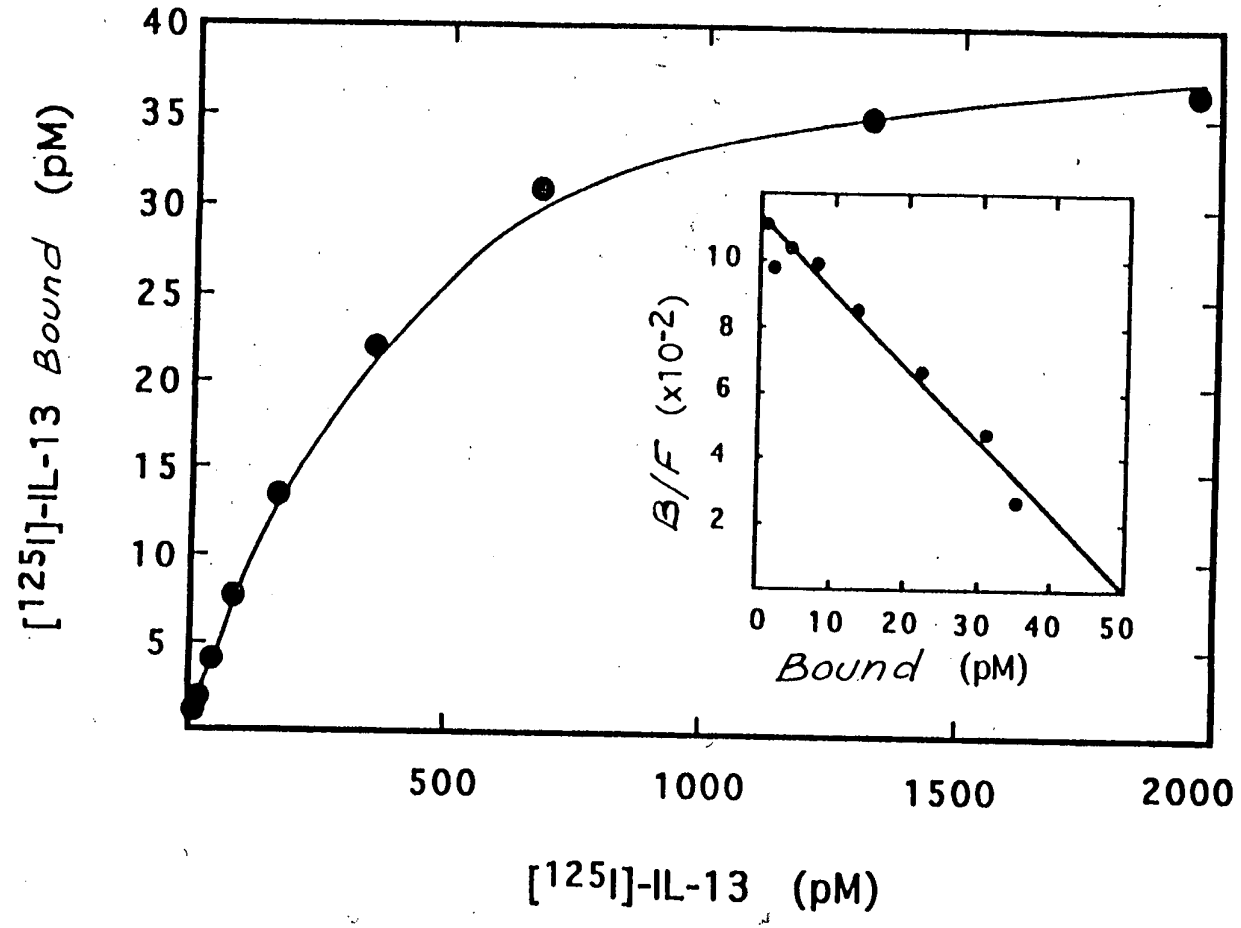
40
35
30
25
20
15
10
5
[125I]-IL-13 Bound (pM)
500
1000
1500
2000
[125I]-IL-13 (pM)
B/F (x10-2)
10
8
6
4
2
0 10 20 30 40 50
Bound (pM)

FIG. 1ØA

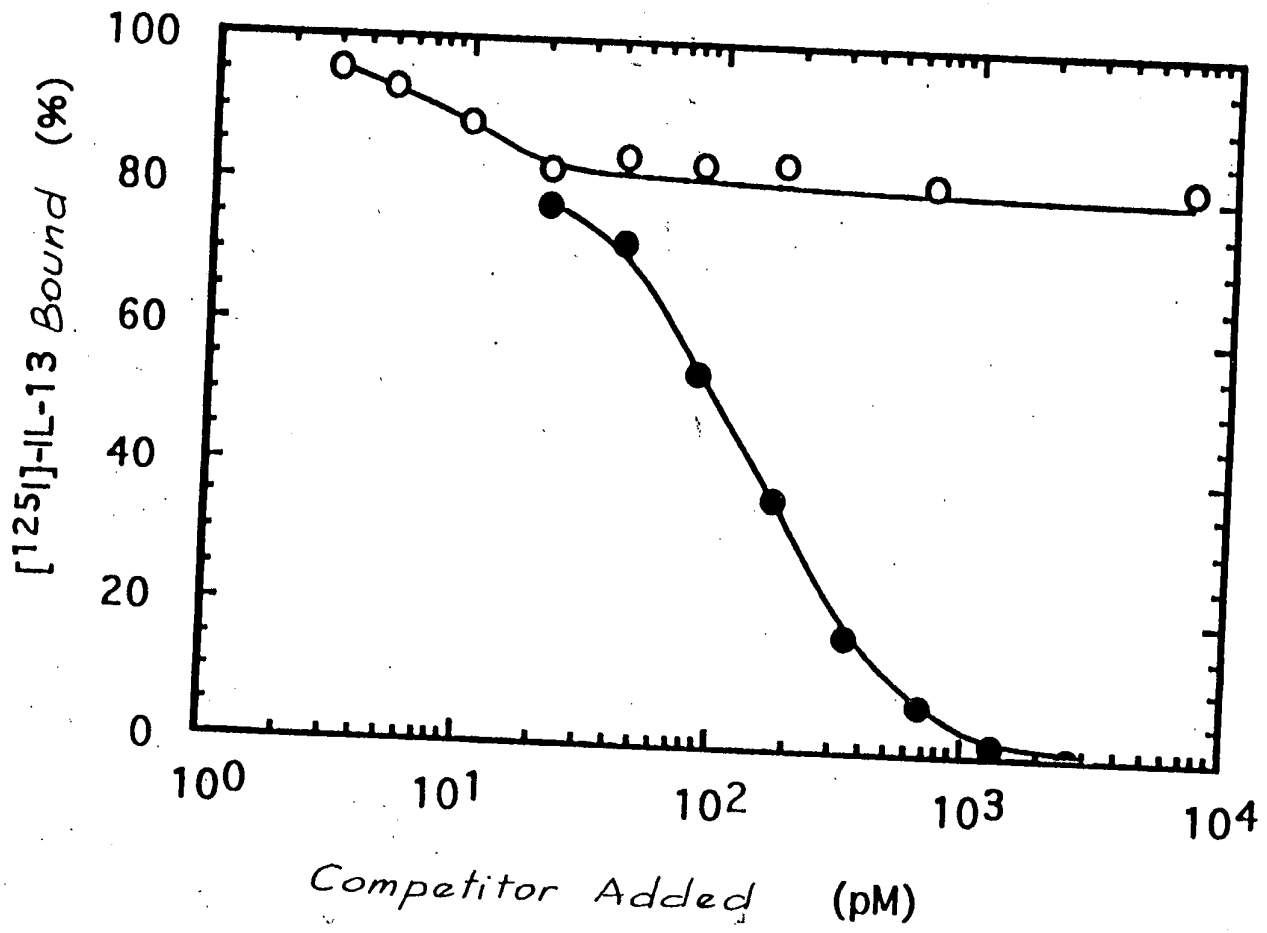
100
80
60
40
20
0
[125I]-IL-13 Bound (%)
100
101
102
103
104
Competitor Added (pM)

FIG. 1B

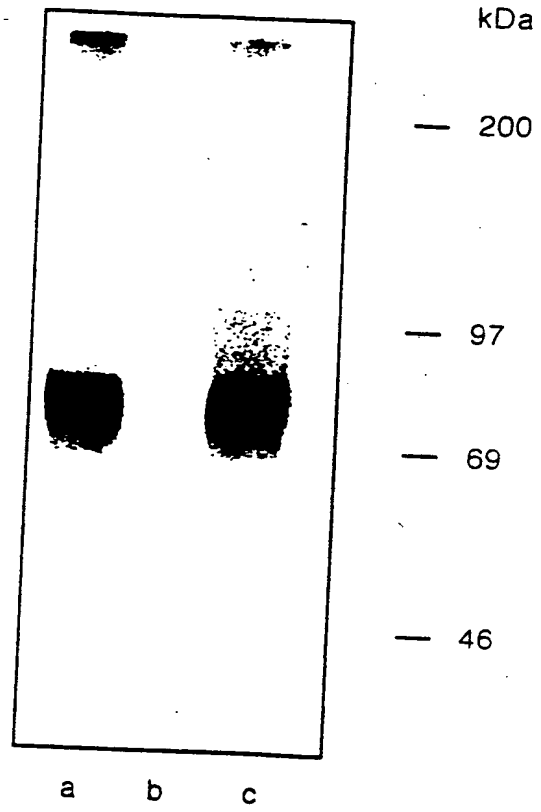

FIG. 1 C

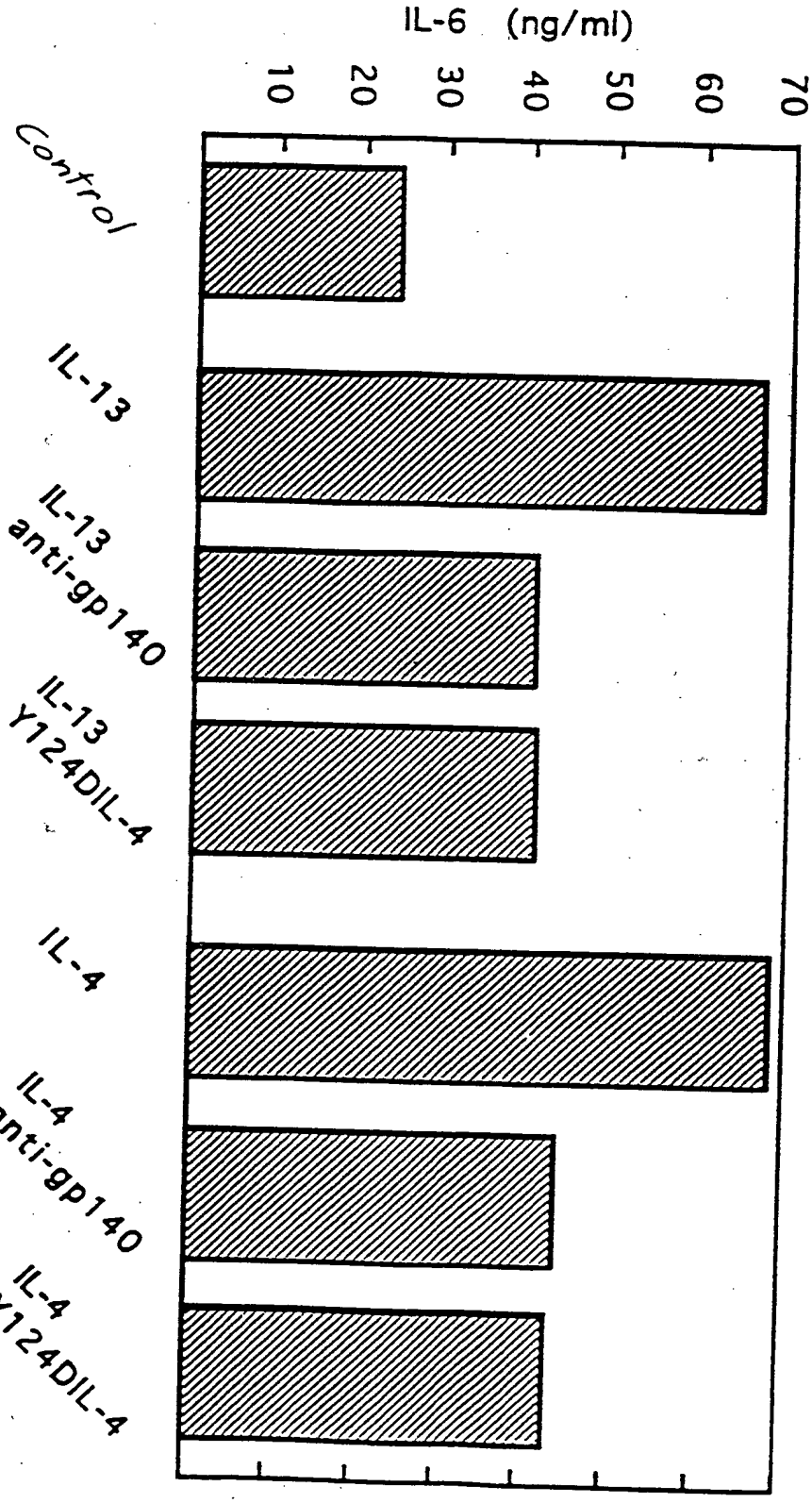
IL-6 (ng/ml)
10
20
30
40
50
60
70
Control
IL-13
IL-13 anti-gp140
IL-13 Y124DIL-4
IL-4
IL-4 anti-gp140
IL-4 Y124DIL-4

FIG. 1ØD

```
1    GGTGCCTGTCGGCGGGGAGAGAGGCAATATCAAGGTTTTAAATCTCGGAGAAATGGCT   58
1                                                        MetAla     2

59   TTCGTTTGCTTGGCTATCGGATGCTTATATACCTTTCTGATAAGCACAACATTTGGCTGT  118
3    PheValCysLeuAlaIleGlyCysLeuTyrThrPheLeuIleSerThrThrPheGlyCys   22

119  ACTTCATCTTCAGACACCGAGATAAAAGTTAACCCTCCTCAGGATTTTGAGATAGTGGAT  178
23   ThrSerSerSerAspThrGluIleLysValAsnProProGlnAspPheGluIleValAsp   42

179  CCCGGATACTTAGGTTATCTCTATTTGCAATGGCAACCCCCACTGTCTCTGGATCATTTT  238
43   ProGlyTyrLeuGlyTyrLeuTyrLeuGlnTrpGlnProProLeuSerLeuAspHisPhe   62

239  AAGGAATGCACAGTGGAATATGAACTAAAATACCGAAACATTGGTAGTGAAACATGGAAG  298
63   LysGluCysThrValGluTyrGluLeuLysTyrArgAsnIleGlySerGluThrTrpLys   82

299  ACCATCATTACTAAGAATCTACATTACAAAGATGGGTTTGATCTTAACAAGGGCATTGAA  358
83   ThrIleIleThrLysAsnLeuHisTyrLysAspGlyPheAspLeuAsnLysGlyIleGlu  102

359  GCGAAGATACACACGCTTTTACCATGGCAATGCACAAATGGATCAGAAGTTCAAAGTTCC  418
103  AlaLysIleHisThrLeuLeuProTrpGlnCysThrAsnGlySerGluValGlnSerSer  122

419  TGGGCAGAAACTACTTATTGGATATCACCACAAGGAATTCCAGAAACTAAAGTTCAGGAT  478
123  TrpAlaGluThrThrTyrTrpIleSerProGlnGlyIleProGluThrLysValGlnAsp  142

479  ATGGATTGCGTATATTACAATTGGCAATATTTACTCTGTTCTTGGAAACCTGGCATAGGT  538
143  MetAspCysValTyrTyrAsnTrpGlnTyrLeuLeuCysSerTrpLysProGlyIleGly  162

539  GTACTTCTTGATACCAATTACAACTTGTTTTACTGGTATGAGGGCTTGGATCATGCATTA  598
163  ValLeuLeuAspThrAsnTyrAsnLeuPheTyrTrpTyrGluGlyLeuAspHisAlaLeu  182

599  CAGTGTGTTGATTACATCAAGGCTGATGGACAAAATATAGGATGCAGATTTCCCTATTTG  658
183  GlnCysValAspTyrIleLysAlaAspGlyGlnAsnIleGlyCysArgPheProTyrLeu  202
```

FIG. 2a A

```
659  GAGGCATCAGACTATAAAGATTTCTATATTTGTGTTAATGGATCATCAGAGAACAAGCCT  718
203  GluAlaSerAspTyrLysAspPheTyrIleCysValAsnGlySerSerGluAsnLysPro  222

719  ATCAGATCCAGTTATTTCACTTTTCAGCTTCAAAATATAGTTAAACCTTTGCCGCCAGTC  778
223  IleArgSerSerTyrPheThrPheGlnLeuGlnAsnIleValLysProLeuProProVal  242

779  TATCTTACTTTTACTCGGGAGAGTTCATGTGAAATTAAGCTGAAATGGAGCATACCTTTG  838
243  TyrLeuThrPheThrArgGluSerSerCysGluIleLysLeuLysTrpSerIleProLeu  262

839  GGACCTATTCCAGCAAGGTGTTTTGATTATGAAATTGAGATCAGAGAAGATGATACTACC  898
263  GlyProIleProAlaArgCysPheAspTyrGluIleGluIleArgGluAspAspThrThr  282

899  TTGGTGACTGCTACAGTTGAAAATGAAACATACACCTTGAAAACAACAAATGAAACCCGA  958
283  LeuValThrAlaThrValGluAsnGluThrTyrThrLeuLysThrThrAsnGluThrArg  302

959  CAATTATGCTTTGTAGTAAGAAGCAAAGTGAATATTTATTGCTCAGATGACGGAATTTGG  1018
303  GlnLeuCysPheValValArgSerLysValAsnIleTyrCysSerAspAspGlyIleTrp  322

1019 AGTGAGTGGAGTGATAAACAATGCTGGGAAGGTGAAGACCTATCGAAGAAAACTTTGCTA  1078
323  SerGluTrpSerAspLysGlnCysTrpGluGlyGluAspLeuSerLysLysThrLeuLeu  342

1079 CGTTTCTGGCTACCATTTGGTTTCATCTTAATATTAGTTATATTTGTAACCGGTCTGCTT  1138
343  ArgPheTrpLeuProPheGlyPheIleLeuIleLeuValIlePheValThrGlyLeuLeu  362

1139 TTGCGTAAGCCAAACACCTACCCAAAAATGATTCCAGAATTTTTCTGTGATACATGAAGA  1198
363  LeuArgLysProAsnThrTyrProLysMetIleProGluPhePheCysAspThr        381

1199 CTTTCCATATCAAGAGACATGGTATTGACTCAACAGTTTCCAGTCATGGCCAAATGTTCA  1258
1259 ATATGAGTCTCAATAAACTGAATTTTTCTTGCGAATGTTG  1298
```

FIG. 2a(continuation) B

```
IL13R   MAFVCLAIGCLYTFLISTTFGCTSSSDTEIKVNPPQDFEIVDPGYLGYLY 50
 IL5R   ..MIIVAHVLLILLGATEILQADLLPDEKISLLPPVNFTIKVTG.LAQVL 47

IL13R   LQWQPPLSLDHFKECTVEYELKYRNIGSETWKTIITKNLHYKDGFDLNKG 100
 IL5R   LQWKPNPDQEQ.RNVNLEYQVKINAPKEDDYETRITES...KCVTILHKG 93

IL13R   IEAKIHTLLPWQCTNGSEVQSSWAETTYWISPQGIPETKVQDMDCV.... 146
 IL5R   FSASVRTILQ...NDHSLLASSWASAE.LHAPPGSPGTSIVNLTCTTNTT 139

IL13R   ..YYNWQ.....YLLCSWKPGIGVLLDTNYNLFYWYEGLDHALQCVDYIK 189
 IL5R   EDNYSRLRSYQVSLHCTWLVGTDAPEDTQYFLYYRYGSWTE..ECQEYSK 187

IL13R   AD.GQNIGCRFP..YLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIV 236
 IL5R   DTLGRNIACWFPRTFILSKGRDWLSVLVNGSSKHSAIRPFDQLFALHAID 237

IL13R   KPLPPVYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIEIREDDTTLVTA 286
 IL5R   QINPPLNVTAEIEGT.RLSIQWEKPVSAFPIHCFDYEVKIHNTRNGYLQI 286

IL13R   TVENETYTLKTTNETRQLCFVVRSKVNIYCSDDGIWSEWSDKQCWEGEDL 336
 IL5R   EKLMTNAFISIIDDLSKYDVQVRAAVSSMCREAGLWSEWSQ.PIYVGNDE 335

IL13R   SKKTLLRFWLPFGFILILVIFVTGLLLRKPNTYPKMIP.....EF 376
 IL5R   HKPLREWFVIVIMATICFILLILSLICKICHLWIKLFPPIPAPKSNIKDL 385

IL13R   FCDT..... 380
 IL5R   FVTTNYEKAGSSETEIEVICYIEKPGVETLEDSVF 420
```

FIG. 2B C

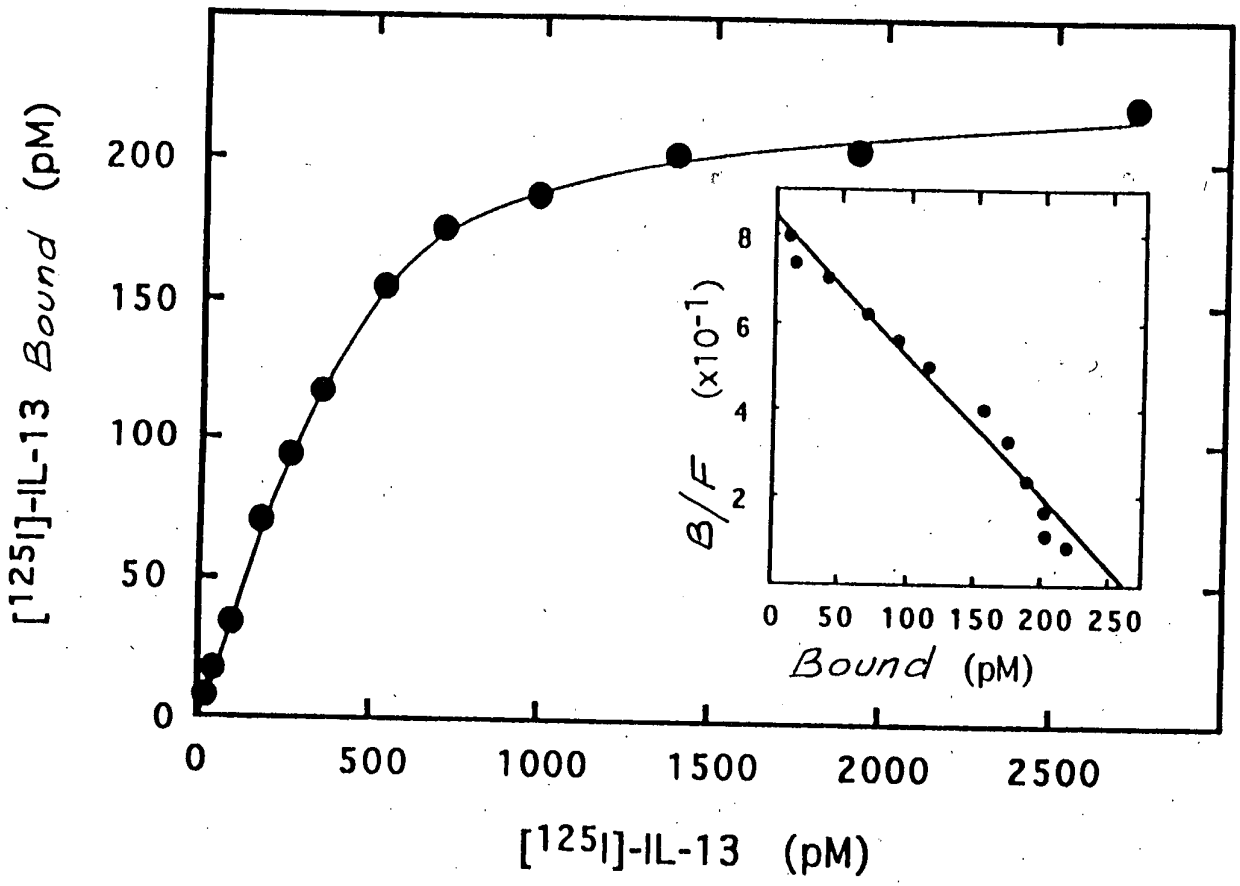
[125I]-IL-13 Bound (pM)
200
150
100
50
0
0
500
1000
1500
2000
2500
[125I]-IL-13 (pM)
B/F (x10-1)
8
6
4
2
0
50
100
150
200
250
Bound (pM)

FIG. 4ØA

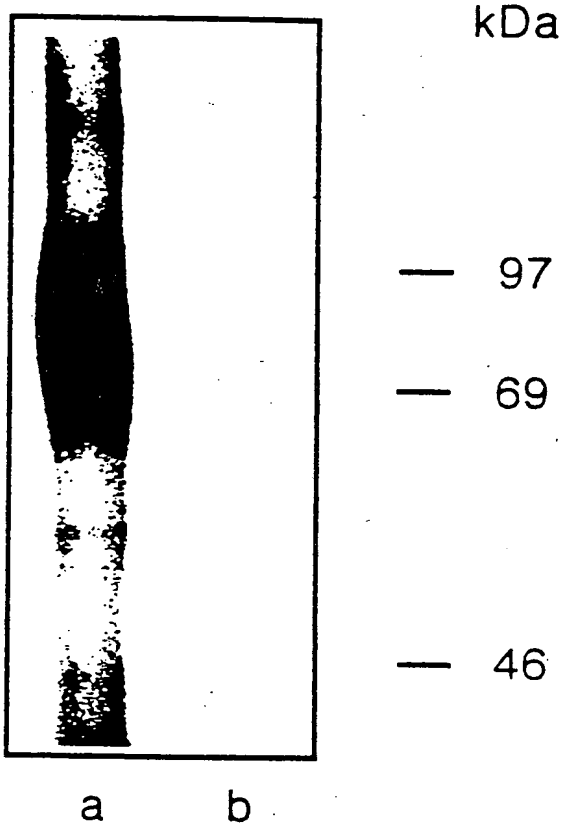

FIG. 4B

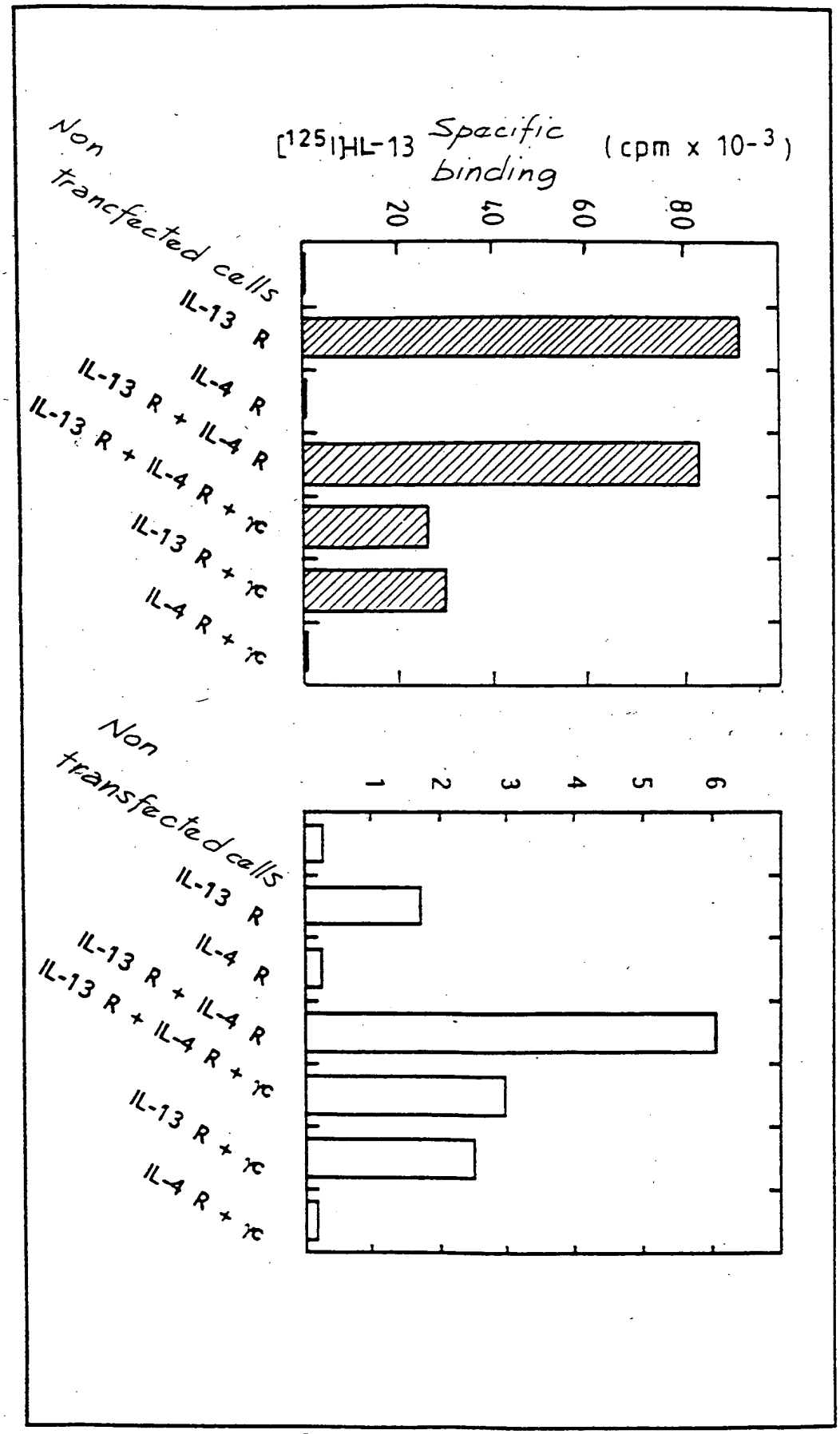
[125I]HL-13 Specific binding (cpm x 10-3)
20
40
60
80
Non transfected cells
IL-13 R
IL-4 R
IL-13 R + IL-4 R
IL-13 R + IL-4 R + γc
IL-13 R + γc
IL-4 R + γc
Non transfected cells
1
2
3
4
5
6
IL-13 R
IL-4 R
IL-13 R + IL-4 R
IL-13 R + IL-4 R + γc
IL-13 R + γc
IL-4 R + γc

FIG.4C

Specific binding
[125I]IL-4 (cpm x 10-3)
1.4
1.2
1.0
0.8
0.6
0.4
0.2
Non transfected cells
IL-13 R
IL-4 R
IL-13 R + IL-4 R
IL-13 R + IL-4 R + γc
IL-13 R + γc
IL-4 R + γc
Non transfected cells
15
10
5
IL-13 R
IL-4 R
IL-13 R + IL-4 R
IL-13 R + IL-4 R + γc
IL-13 R + γc
IL-4 R + γc

FIG. 4D

```
   1  TCAGCCCGGCCGGGCTCCGAGGCGAGAGGCTGCATGGAGTGGCCGGCGCGGCTCTGCGGG   60
 -10                                    M  E  W  P  A  R  L  C  G      9
  61  CTGTGGGCGCTGCTGCTCTGCGCCGGCGGCGGGGGCGGGGGCGGGGGCGCCGCGCCTACG  120
  10  L  W  A  L  L  L  C  A  G  G  G  G  G  G  G  G  A  A  P  T     29
 121  GAAACTCAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTGCACAGTAATA  180
  30  E  T  Q  P  P  V  T [N  L  S  V] S  V  E  N  L  C  T  V  I     49
 181  TGGACATGGAATCCACCCGAGGGAGCCAGCTCAAATTGTAGTCTATGGTATTTTAGTCAT  240
  50  W  T  W  N  P  P  E  G  A  S  S [N  C  S  L] W  Y  F  S  H     69
 241  TTTGGCGACAAACAAGATAAGAAAATAGCTCCGGAAACTCGTCGTTCAATAGAAGTACCC  300
  70  F  G  D  K  Q  D  K  K  I  A  P  E  T  R  R  S  I  E  V  P     89
 301  CtGAATGAGAGGATTTGTCTGCAAGTGGGGTCCCAGTGTAGCACCAATGAGAGTGAGAAG  360
  90  L  N  E  R  I  C  L  Q  V  G  S  Q  C  S  T [N  E  S  E] K    109
 361  CCTAGCATTTTGGTTGAAAAATGCATCTCACCCCCAGAAGGTGATCCTGAGTCTGCTGTG  420
 110  P  S  I  L  V  E  K  C  I  S  P  P  E  G  D  P  E  S  A  V    129
 421  ACTGAGCTTCAATGCATTTGGCACAACCTGAGCTACATGAAGTGTTCTTGGCTCCCTGGA  480
 130  T  E  L  Q  C  I  W  H [N  L  S  Y] M  K  C  S  W  L  P  G    149
 481  AGGAATACCAGTCCCGACACTAACTATACTCTCTACTATTGGCACAGAAGCCTGGAAAAA  540
 150  R  N  T  S  P  D  T [N  Y  T  L] Y  Y  W  H  R  S  L  E  K    169
 541  ATTCATCAATGTGAAAACATCTTTAGAGAAGGCCAATACTTTGGTTGTTCCTTTGATCTG  600
 170  I  H  Q  C  E  N  I  F  R  E  G  Q  Y  F  G  C  S  F  D  L    189
 601  ACCAAAGTGAAGGATTCCAGTTTtGAACAACACAGTGTCCAAATAATGGTCAAGGATAAT  660
 190  T  K  V  K  D  S  S  F  E  Q  H  S  V  Q  I  M  V  K  D  N    209
 661  GCAGGAAAAATTAAACCATCCTTCAATATAGTGCCTTTAACTTCCCGTGTGAAACCTGAT  720
 210  A  G  K  I  K  P  S  F  N  I  V  P  L  T  S  R  V  K  P  D    229
 721  CCTCCACATATTAAAAACCTCTCCTTCCACAATGATGACCTATATGTGCAATGGGAGAAT  780
 230  P  P  H  I  K [N  L  S  F] H  N  D  D  L  Y  V  Q  W  E  N    249
 781  CCACAGAATTTTATTAGCAGATGCCTATTTTATGAAGTAGAAGTCAATAACAGCCAAACT  840
 250  P  Q  N  F  I  S  R  C  L  F  Y  E  V  E  V [N  N  S  Q] T    269
 841  GAGACACATAATGTTTTCTACGTCCAAGAGGCTAAATGTGAGAATCCAGAATTTGAGAGA  900
 270  E  T  H  N  V  F  Y  Y  V  Q  E  A  K  C  E  N  P  E  F  E  R  289
 901  AATGTGGAGAATACATCTTGTTTCATGGTCCCTGGTGTTCTTCCTGATACTTTGAACACA  960
 290  N  V  E [N  T  S  C] F  M  V  P  G  V  L  P  D  T  L  N  T    309
 961  GTCAGAATAAGAGTCAAAACAAATAAGTTATGCTATGAGGATGACAAACTCTGGAGTAAT 1020
 310  V  R  I  R  V  K  T  N  K  L  C  Y  E  D  D  K  L  W  S [N    329
1021  TGGAGCCAAGAAATGAGTATAGGTAAGAAGCGCAATTCCACACTCTACATAACCATGTTA 1080
 330  W  S  Q] E  M  S  I  G  K  K  R [N  S  T  L] Y  I  T  M  L    349
1081  CTCATTGTTCCAGTCATCGTCGCAGGTGCAATCATAGTACTCCTGCTTTACCTAAAAAGG 1140
 350  L  I  V  P  V  I  V  A  G  A  I  I  V  L  L  L  Y  L  K  R    369
1141  CTCAAGATTATTATATTCCCTCCAATTCCTGATCCTGGCAAGATTTTTAAAGAAATGTTT 1200
 370  L  K  I  I  I  F  P  P  I  P  D  P  G  K  I  F  K  E  M  F    389
1201  GGAGACCAGAATGATGATACTCTGCACTGGAAGAAGTACGACATCTATGAGAAGCAAACC 1260
 390  G  D  Q  N  D  D  T  L  H  W  K  K  Y  D  I  Y  E  K  Q  T    409
1261  AAGGAGGAAACCGACTCTGTAGTGCTGATAGAAAACCTGAAGAAAGCCTCTCAGTGATGG 1320
 410  K  E  E  T  D  S  V  V  L  I  E  N  L  K  K  A  S  Q  *      429
```

FIG. 7a A

```
1381  TATCTGGGAACTTATTAAATGGAAACTGAAACTACTGCACCATTTAAAAACAGGCAGCTC  1440
1441  ATAAGAGCCACAGGTCTTTATGTTGAGTCGCGCACCGAAAAACTAAAAATAATGGGCGCT  1500
1501  TTGGAGAAGAGTGTGGAGTCATTCTCATTGAATTATAAAAGCCAGCAGGCTTCAAACTAG  1560
1561  GGGACAAAGCAAAAAGTGATGATAGTGGTGGAGTTAATCTTATCAAGAGTTGTGACAACT  1620
1621  TCCTGAGGGATCTATACTTGCTTTGTGTTCTTTGTGTCAACATGAACAAATTTTATTTGT  1680
1681  AGGGGAACTCATTTGGGGTGCAAATGCTAATGTCAAACTTGAGTCACAAAGAACATGTAG  1740
1741  AAAACAAAATGGATAAAATCTGATATGTATTGTTTGGGATCCTATTGAACCATGTTTGTG  1800
1801  GCTATTAAAACTCTTTTAACAGTCTGGGCTGGGTCCGGTGGCTCACGCCTGTAATCCCAG  1860
1861  CAATTTGGGAGTCCGAGGCGGGCGGATCACTCGAGGTCAGGAGTTCCAGACCAGCCTGAC  1920
1921  CAAAATGGTGAAACCTCCTCTCTACTAAAACTACAAAAATTAACTGGGTGTGGTGGCGCG  1980
1981  TGCCTGTAATCCCAGCTACTCGGGAAGCTGAGGCAGGTGAATTGTTTGAACCTGGGAGGT  2040
2041  GGAGGTTGCAGTGAGCAGAGATCACACCACTGCACTCTAGCCTGGGTGACAGAGCAAGAC  2100
2101  TCTGTCTAAAAAAACAAAACAAAACAAAACAAAACAAAAAAACCTCTTAATATTCTGGAGT  2160
2161  CATCATTCCCTTCGACAGCATTTTCCTCTGCTTTGAAAGCCCCAGAAATCAGTGTTGGCC  2220
2221  ATGATGACAACTACAGAAAAACCAGAGGCAGCTTCTTTGCCAAGACCTTTCAAAGCCATT  2280
2281  TTAGGCTGTTAGGGGCAGTGGAGGTAgAATGACTCCTTGGGTATTAGAGTTTCAACCATG  2340
2341  AAGTCTCTAACAATGTaTTTTCTTCACCTCTGCTACTCAAGTAGCATTTACTGTGTCTTT  2400
2401  GGTTTGTGCTAGGCCCCCGGGTGTGAAGCACAGACCCCTTCCAGGGGTTTACAGTCTATt  2460
2461  TGAGACTCCTCAGTTCTTGCCACTTTTTTTTTTAATCTCCACCAGTCATTTTTCAGACCT  2520
2521  TTTAACTCCTCAATTCCAACACTGATTTCCCCTTTTGCATTCTCCCTCCTTCCCTTCCTT  2580
2581  GTAGCCTTTTGACTTTCATTGGAAATTAGGATGTAAATCTGCTCAGGAGACCTGGAGGAG  2640
2641  CAGAGGATAATTAGCATCTCAGGTTAAGTGTGAGTAATCTGAGAAACAATGACTAATTCT  2700
2701  TGCATATTTTGTAACTTCCATGTGAGGGTTTTCAGCATTGATATTTGTGCATTTTCTAAA  2760
2761  CAGAGATGAGGTGGTATCTTCACGTAGAACATTGGTATTCGCTTGAGAAAAAAAGAATAG  2820
2821  TTGAACCTATTTCTCTTTCTTTACAAGATGGGTCCAGGATTCCTCTTTTCTCTGCCATAA  2880
2881  ATGATTAATTAAATAGCTTTTGTGTCTTACATTGGTAGCCAGCCAGCCAAGGCTCTGTTT  2940
2941  ATGCTTTTGGGGGGCATATATTGGGTTCCATTCTCACCTATCCACACAACATATCCGTAT  3000
3001  ATATCCCCTCTACTCTTACTTCCCCCAAATTTAAAGAAGTATGGGAAATGAGAGGCATTT  3060
3061  CCCCCACCCCATTTCTCTCCTCACACACAGACTCATATTACTGGTAGGAACTTGAGAACT  3120
3121  TTATTTCCAAGTTGTTCAAACATTTACCAATCATATTAATACAATGATGCTATTTGCAAT  3180
3181  TCCTGCTCCTAGGGGAGGGGAGATAAGAAACCCTCACTCTCTACAGGTTTGGGTACAAGT  3240
3241  GGCAACCTGCTTCCATGGCCGTGTAGAAGCATGGTGCCCTGGCTTCTCTGAGGAAGCTGG  3300
3301  GGTTCATGACAATGGCAGATGTAAAGTTATTCTTGAAGTCAGATTGAGGCTGGGAGACAG  3360
3361  CCGTAGTAGATGTTCTACTTTGTTCTGCTGTTCTCTAGAAAGAATATTTGGTTTTCCTGT  3420
3421  ATAGGAATGAGATTAATTCCTTTCCAGGTATTTTATAATTCTGGGAAGCAAAACCCATGC  3480
3481  CTCCCCCTAGCCATTTTTACTGTTATCCTATTTAGATGGCCATGAAGAGGATGCTGTGAA  3540
3541  ATTCCCAACAAACATTGATGCTGACAGTCATGCAGTCTGGGAGTGGGGAAGTGATCTTTT  3600
3601  GTTCCCATCCTCTTCTTTTAGCAGTAAAATAGCTGAGGGAAAAGGGAGGGAAAAGGAAGT  3660
3661  TATGGGAATACCTGTGGTGGTTGTGATCCCTAGGTCTTGGGAGCTCTTGGAGGTGTCTGT  3720
3721  ATCAGTGGATTTCCCATCCCCTGTGGGAAATTAGTAGGCTCATTTACTGTTTTAGGTCTA  3780
3781  GCCTATGTGGATTTTTTCCTAACATACCTAAGCAAACCCAGTGTCAGGATGGTAATTCTT  3840
3841  ATTCTTTCGTTCAGTTAAGTTTTTCCCTTCATCTGGGCACTGAAGGGATATGTGAAACAA  3900
3901  TGTTAACATTTTTGGTAGTCTTCAACCAGGGATTGTTTCTGTTTAACTTCTTATAGGAAA  3960
3961  GCTTGAGTAAAATAAATATTGTCTTTTTGTATGTCACCCaaaaaaaaaa  4009
```

FIG. 7a(continuation) B

IL-13α MOUSE
HUMAN
IL-13α HUMAN
MOUSE

```
 1 MEWPARLCGLWALLLCAGGGGGGGAAPTETQPPVTNLSVSVENLCTVIW 50
   |.:|| |.:|:.|||   .:.:|..||:||.|||||||||||||||:||
 1 MARPALLGELLVLLL..WTATVGQVAAATEVQPPVTNLSVSVENLCTIIW 48

51 TWNPPEGASSNCSLWYFSHFGDKQDKKIAPETRRSIEVPLNERICLQVGS 100
   ||.||||||.||.|:||||||:|.||||||||||:|. |:||:|:||||||
49 TWSPPEGASPNCTLRYFSHFDDQQDKKIAPETHRKEELPLDEKICLQVGS 98

101 QCSTNESEKPSILVEKCISPPEGDPESAVTELQCIWHNLSYMKCSWLPGR 150
    |||.|||||||| ||.|||||||||||||||.|||||||||||||||||
 99 QCSANESEKPSPLVKKCISPPEGDPESAVTELKCIWHNLSYMKCSWLPGR 148

151 NTSPDTNYTLYYWHRSLEKIHQCENIFREGQYFGCSFDLTKVKDSSFEQH 200
    ||||||:||||||..|||| :|||||:||||.::|||.|||| :.|||::
149 NTSPDTHYTLYYWYSSLEKSRQCENIYREGQHIACSFKLTKV.EPSFEHQ 197

201 SVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDDLYVQWENP 250
    .|||||||||||||:|| .||.||| |||||||||:| :.|:.|.|||.||
198 NVQIMVKDNAGKIRPSCKIVSLTSYVKPDPPHIKHLLLKNGALLVQWKNP 247

251 QNFISRCLFYEVEVNNSQTETHNVFYVQEAKCENPEFERNVENTSCFMVP 300
    ||| |||| |||||||.||: ||:: |:|.||:|.| :||:|.|||| :|
248 QNFRSRCLTYEVEVNNTQTDRHNILEVEEDKCQNSESDRNMEGTSCFQLP 297

301 GVLPDTLNTVRIRVKTNKLCYEDDKLWSNWSQEMSIGKKRNSTLYITMLL 350
    |||:|.: |||:||||||||::|:|||:||:. ||||..|||:|.||||
298 GVLADAVYTVRVRVKTNKLCFDDNKLWSDWSEAQSIGKEQNSTFYTTMLL 347

351 IVPVIVAGAIIVLLLYLKRLKIIIFPPIPDPGKIFKEMFGDQNDDTLHWK 400
    .:||:||.|:|:||:||||||||||||||||||||||||||||||||||||
348 TIPVFVAVAVIILLFYLKRLKIIIFPPIPDPGKIFKEMFGDQNDDTLHWK 397

401 KYDIYEKQTKEETDSVVLIENLKKASQ 427
    ||||||||.||||||||||||||..
398 KYDIYEKQSKEETDSVVLIENLKKAAP 424
```

FIG. 7b C

IL-13α HUMAN

IL-13α MOUSE

```
  1 MEWPARLCGLWALLLCAGGGGGGGGAAPTETQPPVTNLSVSVENLCTVIW 50
    |.:|| |.:|:.|||   .:..|..||:||.|||||||||||||||||:||
  1 MARPALLGELLVLLL..WTATVGQVAAATEVQPPVTNLSVSVENLCTIIW 48

 51 TWNPPEGASSNCSLWYFSHFGDKQDKKIAPETRRSIEVPLNERICLQVGS 100
    ||.||||||.||.|:|||||:|.||||||||||:|. |:||:|:|||||||
 49 TWSPPEGASPNCTLRYFSHFDDQQDKKIAPETHRKEELPLDEKICLQVGS 98

101 QCSTNESEKPSILVEKCISPPEGDPESAVTELQCIWHNLSYMKCSWLPGR 150
    |||.|||||||| ||.|||||||||||||||.|||||||||||||||||||
 99 QCSANESEKPSPLVKKCISPPEGDPESAVTELKCIWHNLSYMKCSWLPGR 148

151 NTSPDTNYTLYYWHRSLEKIHQCENIFREGQYFGCSFDLTKVKDSSFEQH 200
    ||||||:|||||..|||| :|||||:||||.::|||.|||| .:.|||::
149 NTSPDTHYTLYYWYSSLEKSRQCENIYREGQHIACSFKLTKV.EPSFEHQ 197

201 SVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDDLYVQWENP 250
    .||||||||||||:|| .||.||| |||||||||:| :.|:.|.|||.||
198 NVQIMVKDNAGKIRPSCKIVSLTSYVKPDPPHIKHLLLKNGALLVQWKNP 247

251 QNFISRCLFYEVEVNNSQTETHNVFYVQEAKCENPEFERNVENTSCFMVP 300
    ||| |||| |||||||.||: ||:: |:|.||:|.| :||:|.|||| :|
248 QNFRSRCLTYEVEVNNTQTDRHNILEVEEDKCQNSESDRNMEGTSCFQLP 297

301 GVLPDTLNTVRIRVKTNKLCYEDDKLWSNWSQEMSIGKKRNSTLYITMLL 350
    |||:|.: |||:||||||||::|:|||||:||:. ||||..|||:|.||||
298 GVLADAVYTVRVRVKTNKLCFDDNKLWSDWSEAQSIGKEQNSTFYTTMLL 347

351 IVPVIVAGAIIVLLLYLKRLKIIIFPPIPDPGKIFKEMFGDQNDDTLHWK 400
    .:||:||.|:|:||:|||||||||||||||||||||||||||||||||||
348 TIPVFVAVAVIILLFYLKRLKIIIFPPIPDPGKIFKEMFGDQNDDTLHWK 397

401 KYDIYEKQTKEETDSVVLIENLKKASQ 427
    ||||||||.||||||||||||||..
398 KYDIYEKQSKEETDSVVLIENLKKAAP 424
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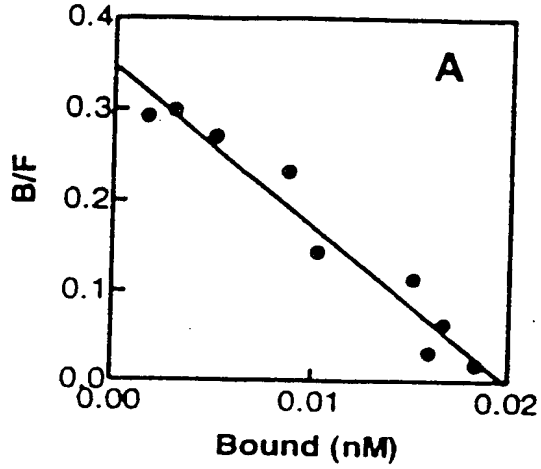
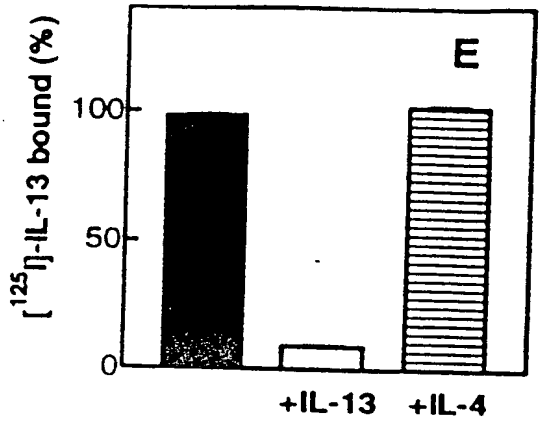
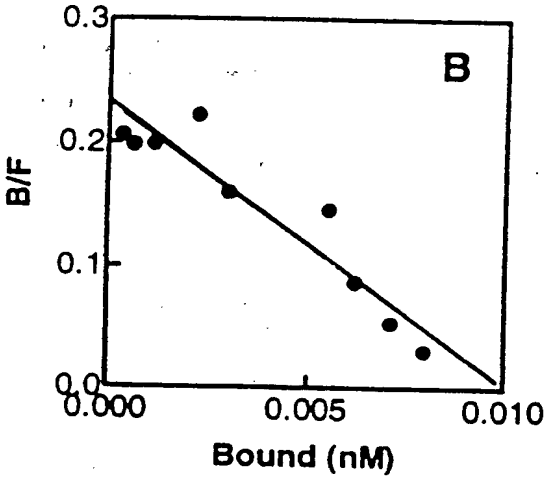
FIG. 7b D


A
B/F
0.4
0.3
0.2
0.1
0.0
0.00
0.01
0.02
Bound (nM)


E
[125I]-IL-13 bound (%)
100
50
0
+IL-13
+IL-4


B
B/F
0.3
0.2
0.1
0.0
0.000
0.005
0.010
Bound (nM)

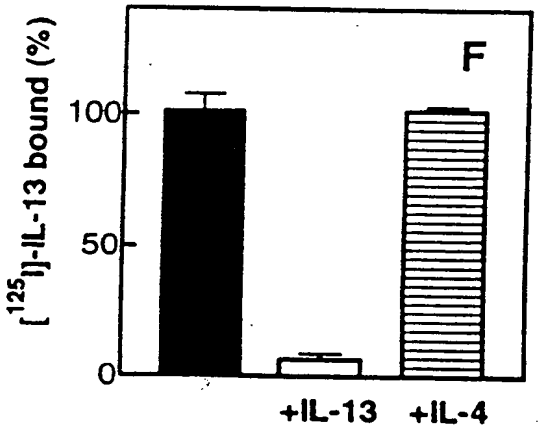
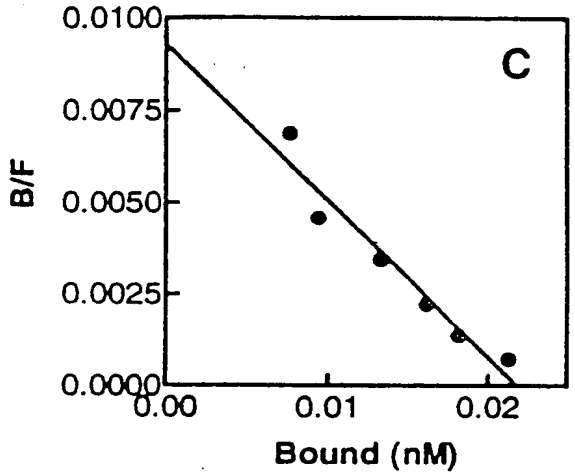
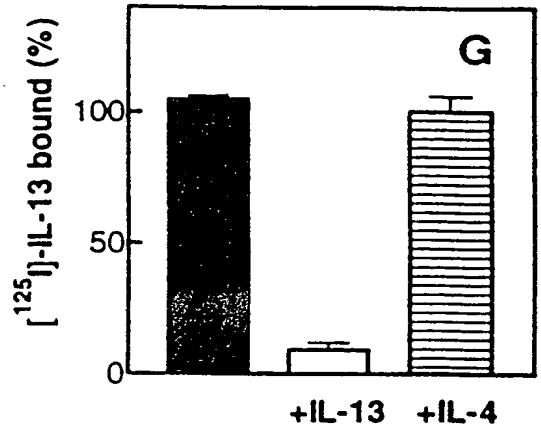
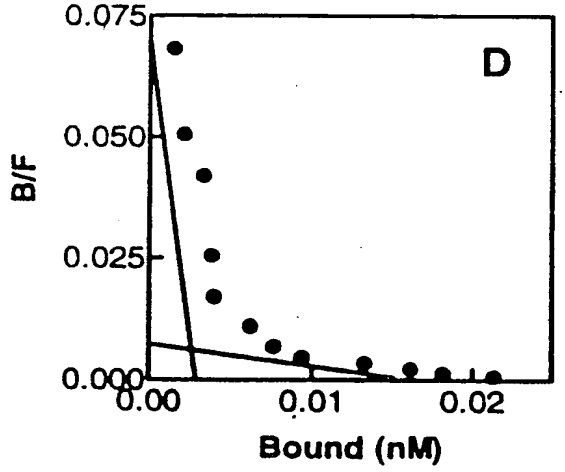

F
[125I]-IL-13 bound (%)
100
50
0
+IL-13
+IL-4

FIG. 8A







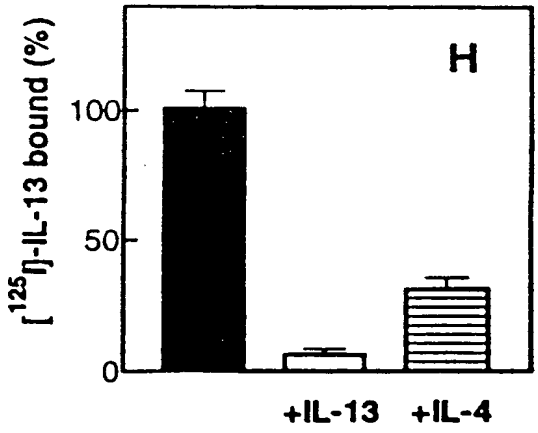


FIG. 8 ~~(continuation)~~ B